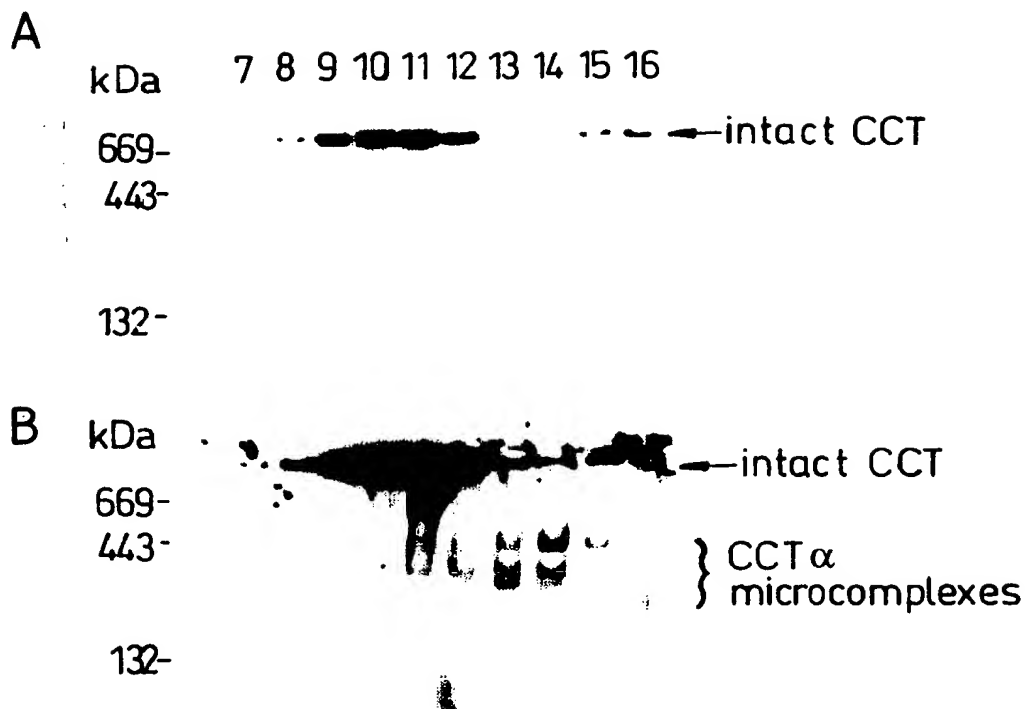


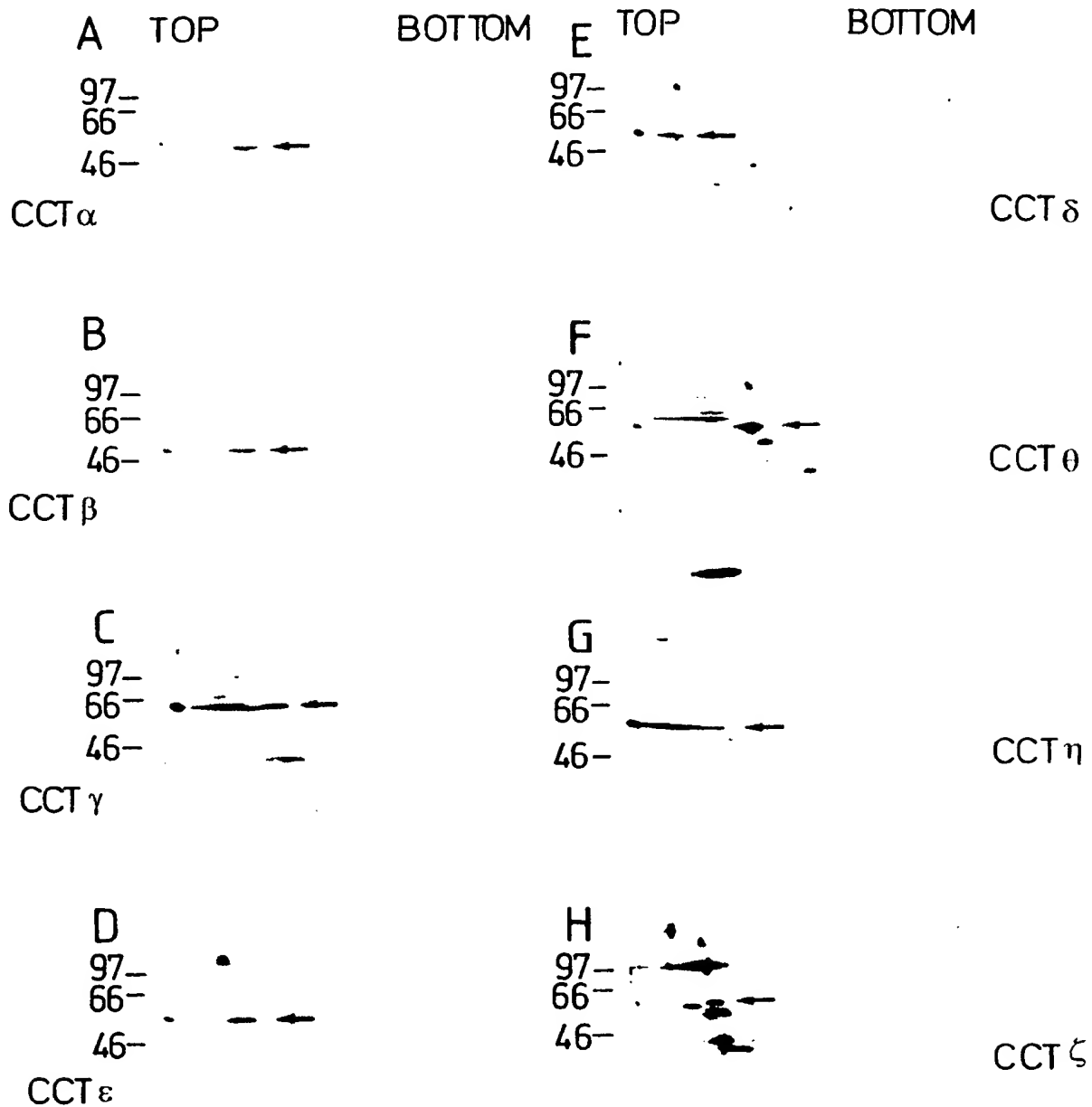
1/19

APPROVED	O.G. FIG.
BY	CLASS
DRAFTSMAN	SUBCLASS

*Fig. 1*

2/19

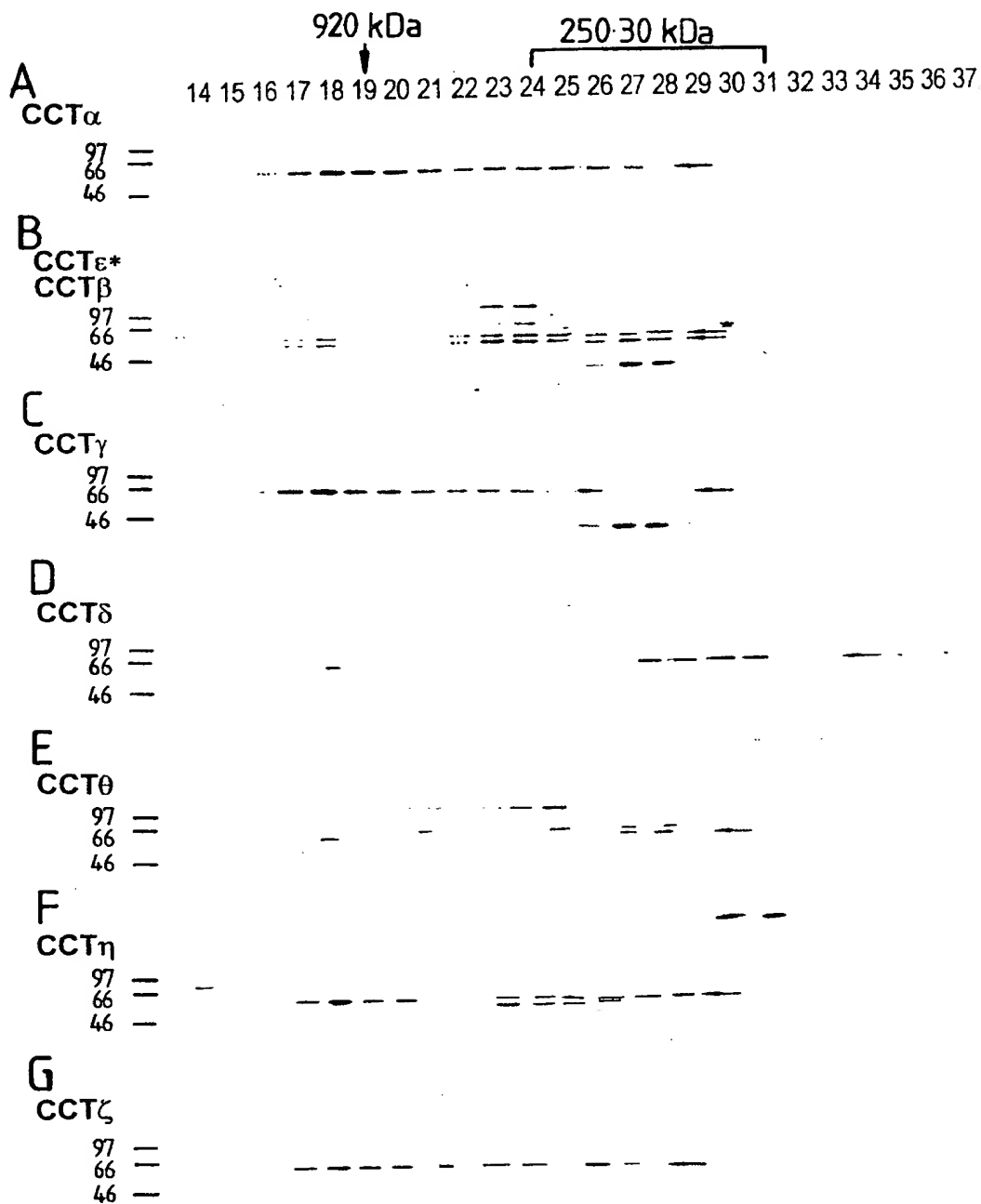
O.G. FIG.	
APPROVED	CLASS SUBCLASS
BY	DRAFTSMAN



**Fig 2**

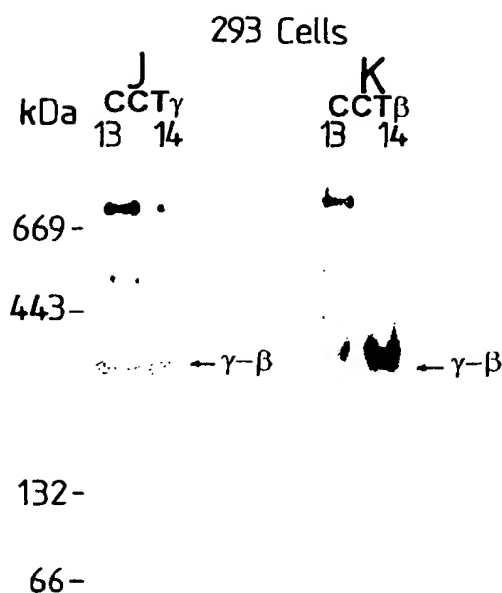
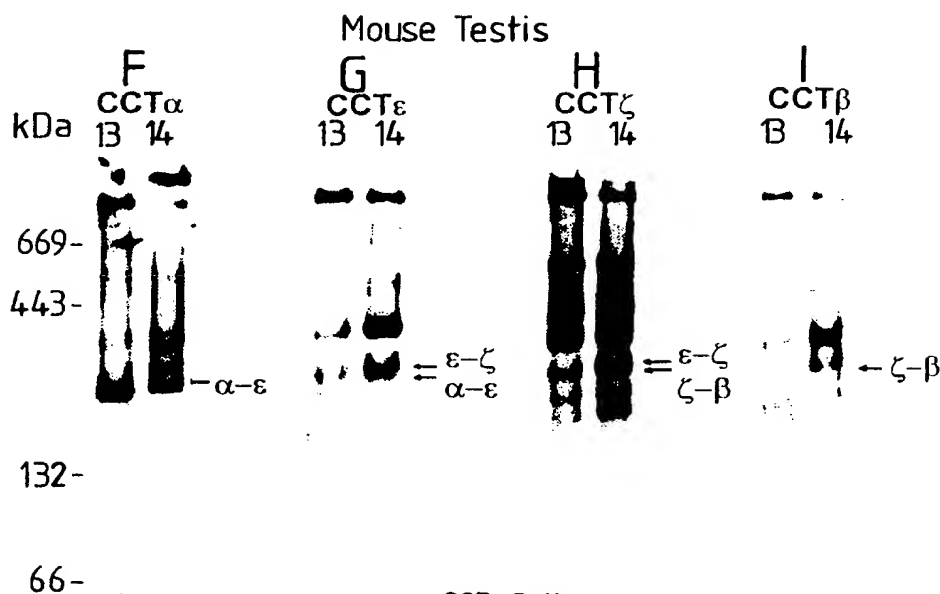
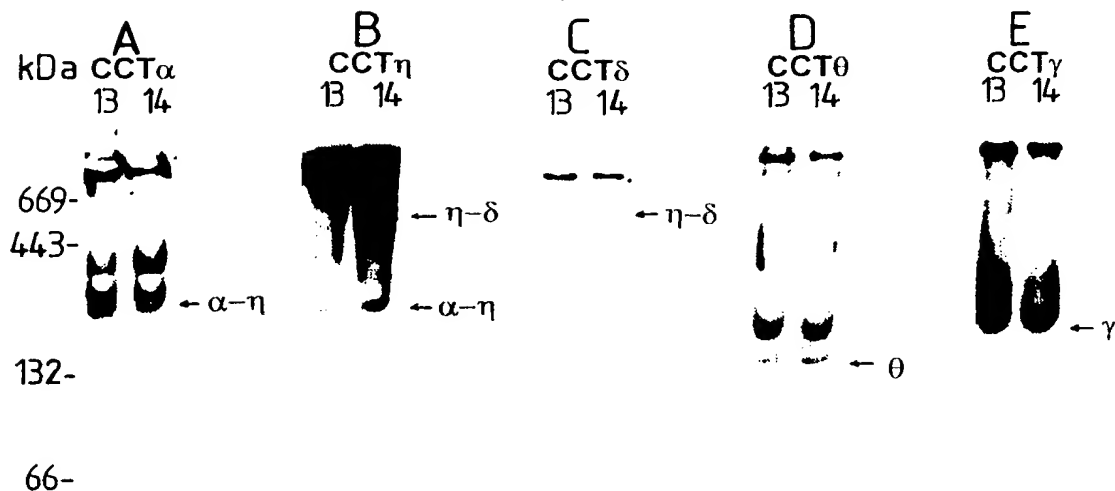
3/19

APPROVED	O.G. FIG.	
	CLASS	SUBCLASS
BY	DRAFTSMAN	

*Fig. 3*

4/19

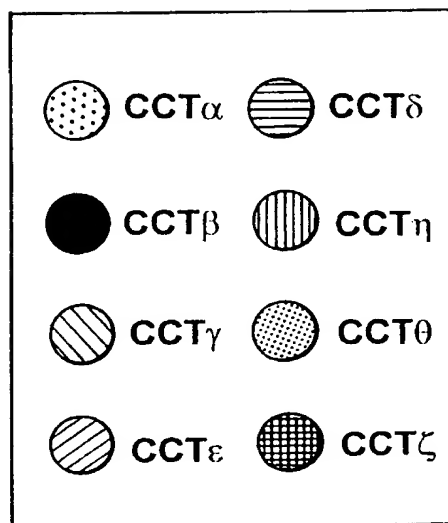
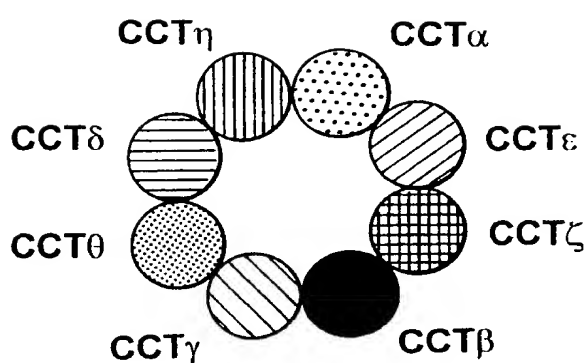
APPROVED	O.C. FIG.	
	CLASS	SUBCLASS
BY		
DRAFTSMAN		



**Fig 4**

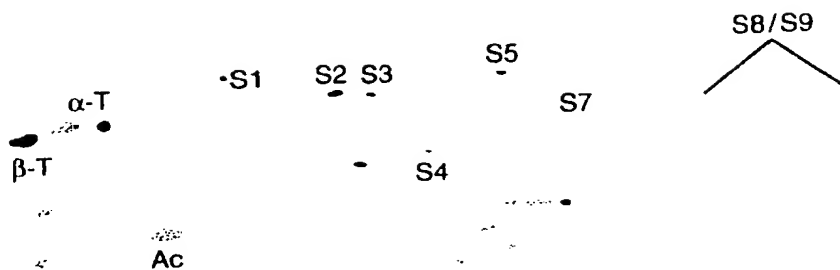
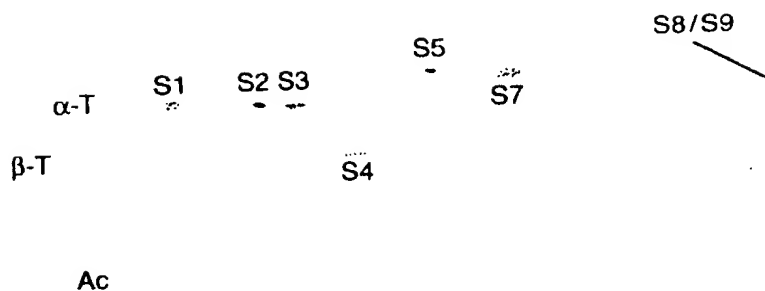
5/19

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

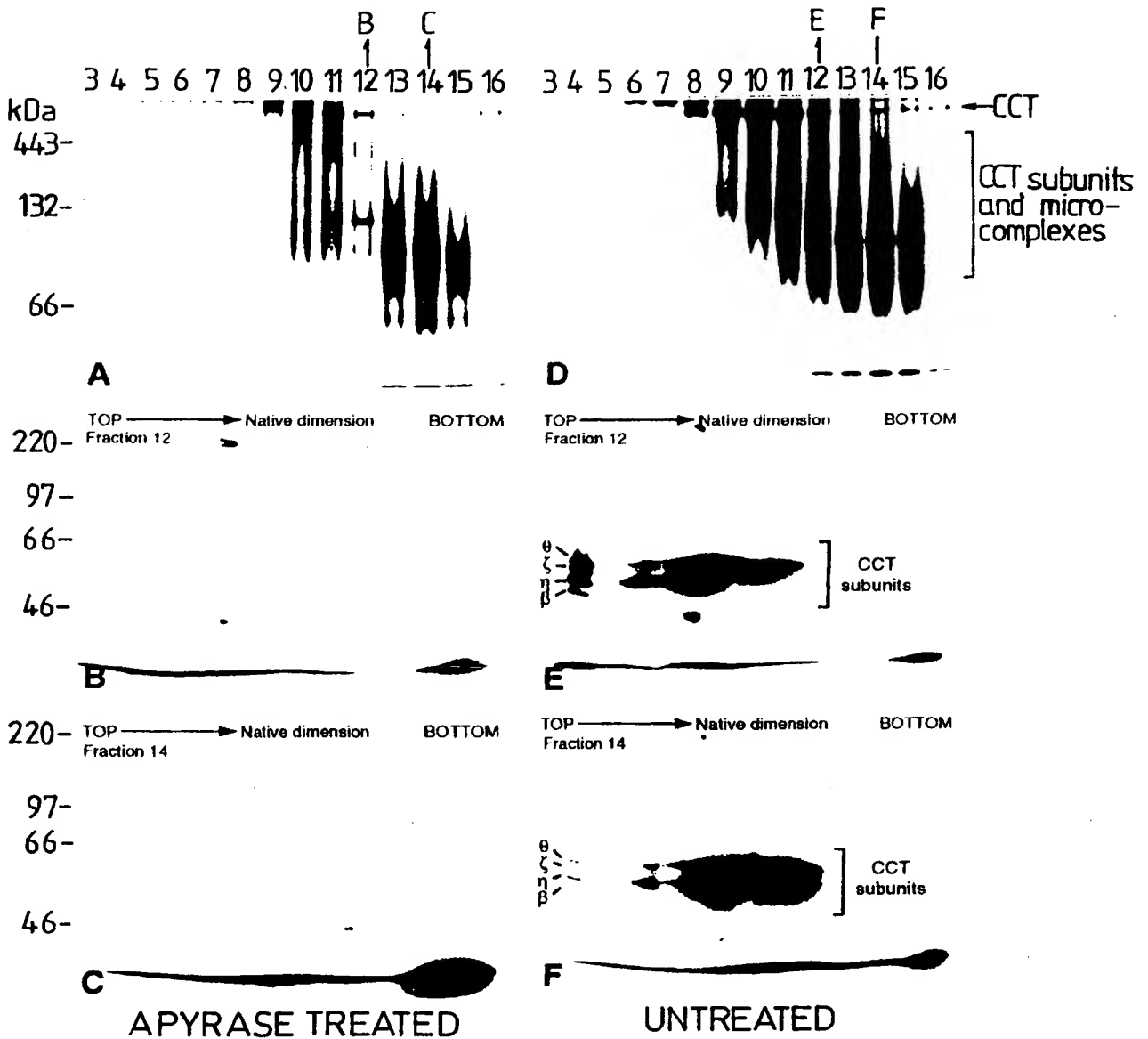
*Fig. 5*

6/19

APPROVED	O.G. FIG.	
	BY	CLASS/SUBCLASS
DRAFTSMAN		

**A****B****C****Fig 6**

7/19

*Fig. 7*

8/19

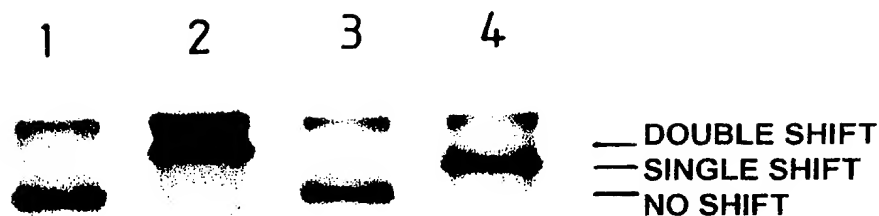
A

Rabbit CCT $\alpha$   
Mouse CCT $\alpha$   
Mutant

...AVHSGAL	D	D
...AVHSGAL	D	D
...AVHSGAL	N	D

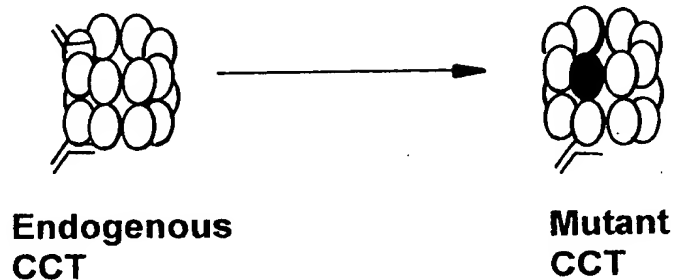
555

B



Two Antibody Molecules  
coupled onto CCT

One Antibody Molecule  
coupled onto CCT



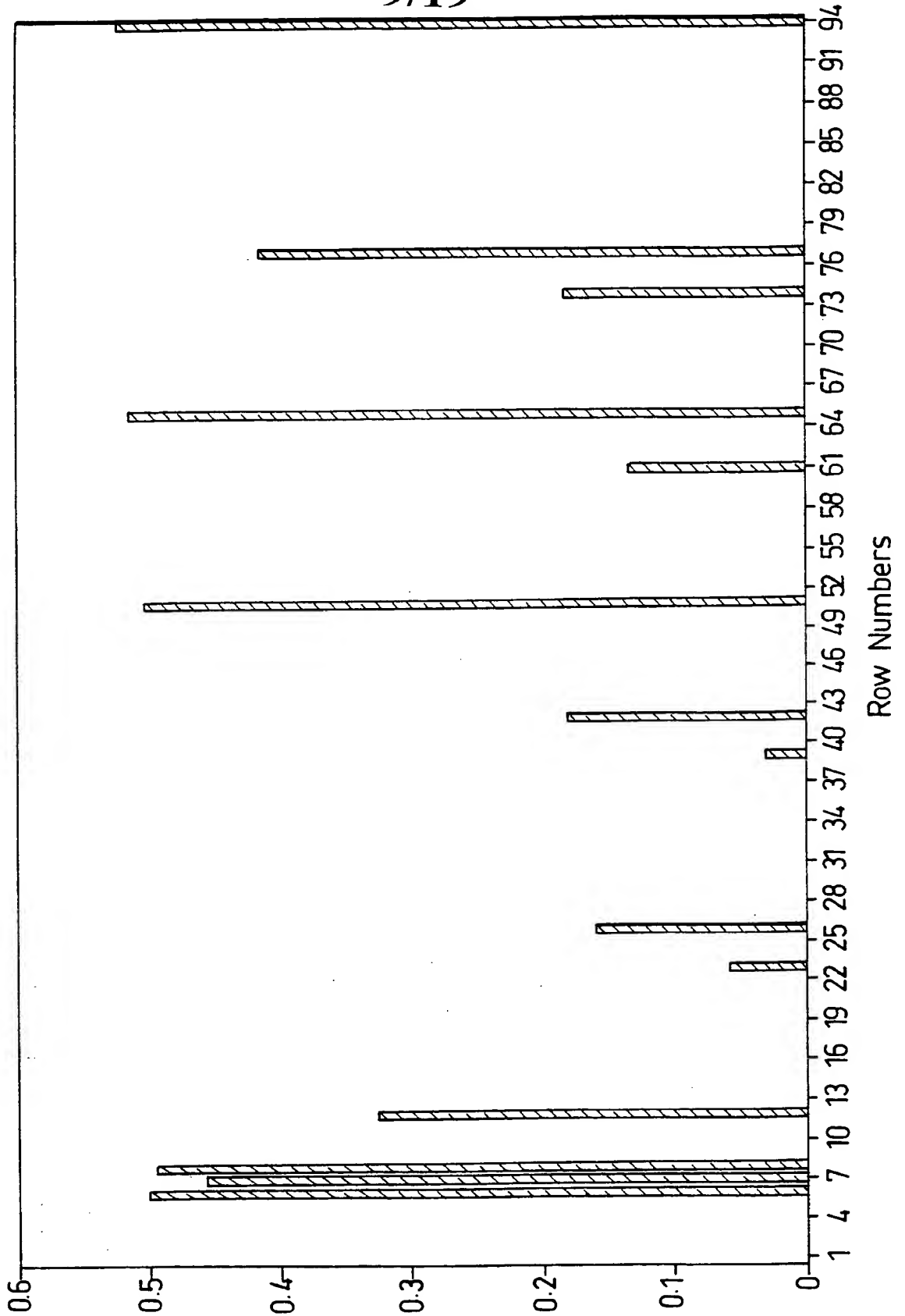
*Fig 8*



APPROVED	O.G.FIG.
BY	CLASS
DRAFTSMAN	SUBCLASS

data/actin PepSet

Fig. 9



10/19

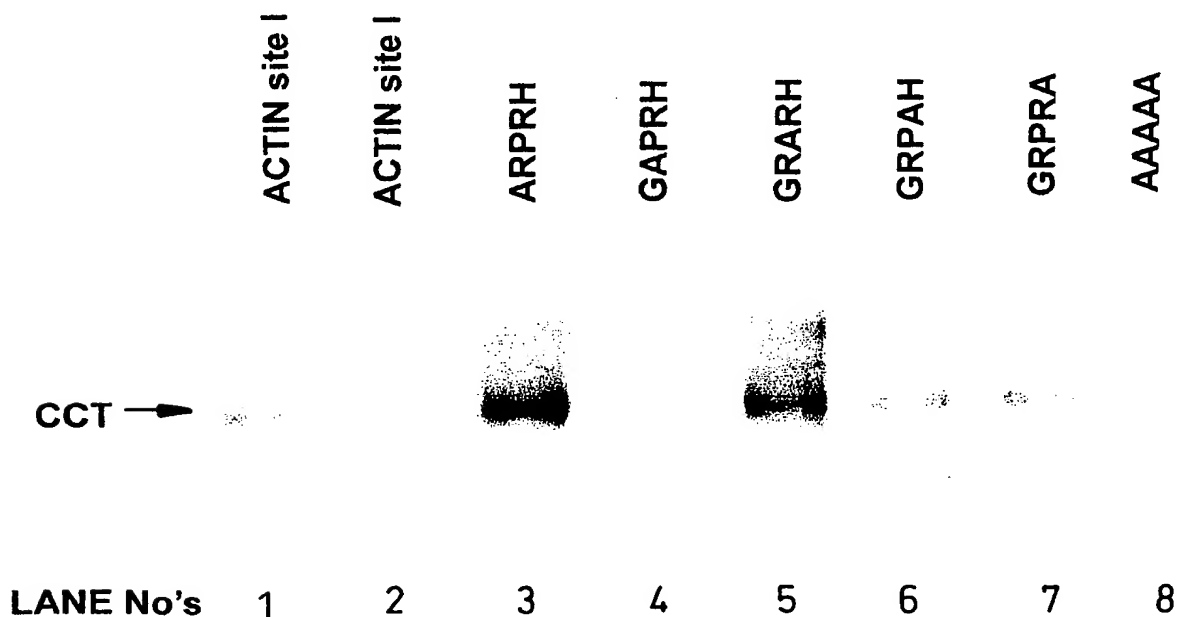
**Fig 10****Peptide Sequences**

Reference Peptide No.	Peptide No. In Figure 11	Peptide Sequence
1	6	APRAVFPSIVGRPRH
2	7	FPSIVGRPRHQGVMV
3	8	GRPRHQGVMVGMGQK
4	61	GGTTMYPGIADRMQK
5	77	PRHQGVMVGMGQKDS
6	26	TFNTPAMYVAIQAVL
7	35	LPHAILRLDLAGRDL
8	70	LASLSTFQQMWISKQ
9	12	DEAQSKRGILTTLKYP
10	28	IQAVLSLYASGRITG
11	39	KILTERGYSFTTTAE
12	40	RGYSFTTTAEREIVR
13	47	ASSSSLEKSYELPDG
14	65	APSTMKIKIIAPPER
15	67	APPERKYSVWIGGSI

APPROVED	O.G. FIG.	
	CLASS	SUBCLASS
BY	DRAFTSMAN	

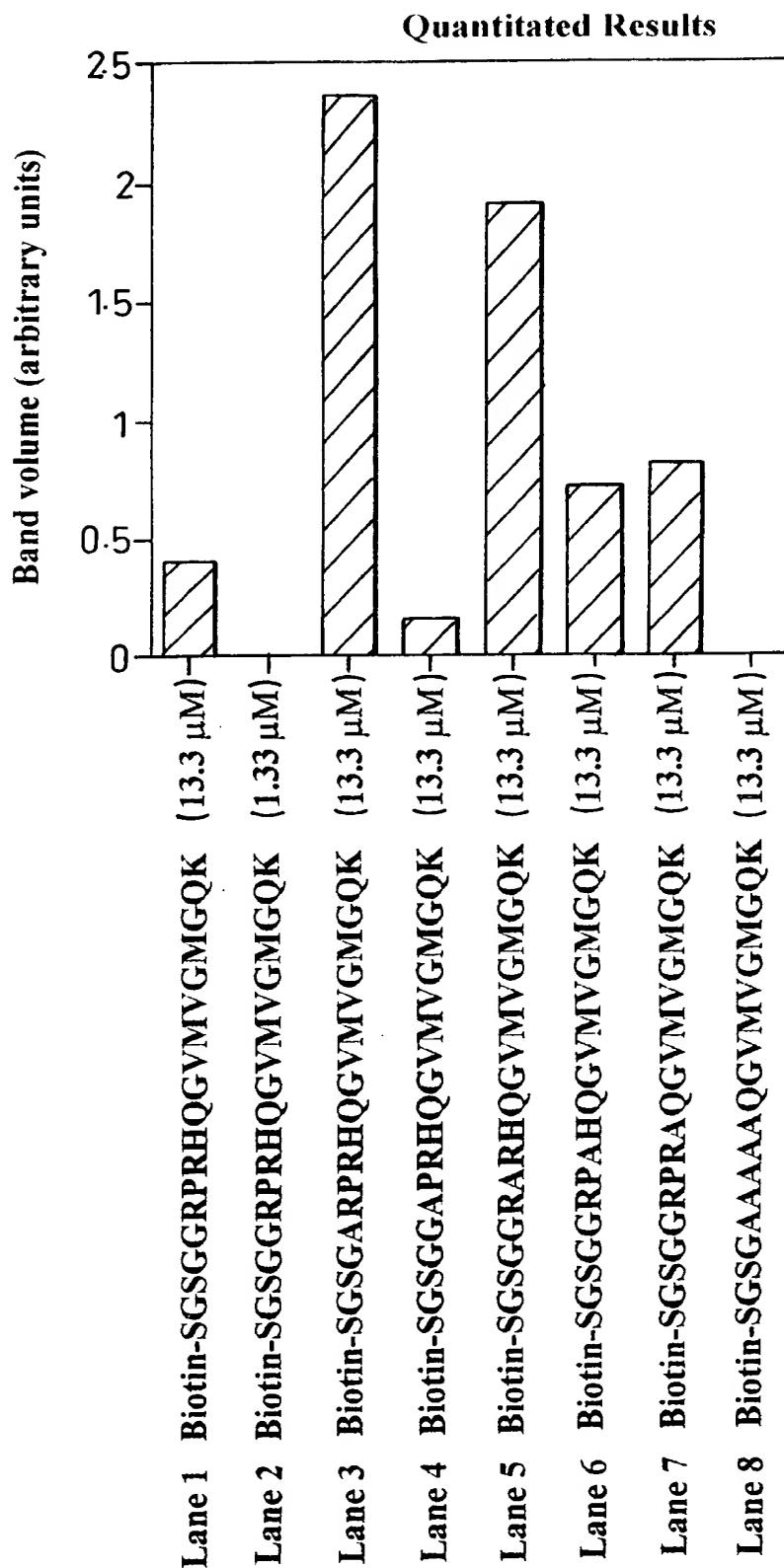
11/19

Lane 1 Peptide 8 at 13.3 $\mu$ M	(Biotin-SGSGGRPRHQGVVMVGMGQK)
Lane 2 Peptide 8 at 1.33 $\mu$ M	(Biotin-SGSGGRPRHQGVVMVGMGQK)
Lane 3 Peptide 8.1 at 13.3 $\mu$ M	(Biotin-SGSGARPRHQGVVMVGMGQK)
Lane 4 Peptide 8.2 at 13.3 $\mu$ M	(Biotin-SGSGGAPRHQGVVMVGMGQK)
Lane 5 Peptide 8.3 at 13.3 $\mu$ M	(Biotin-SGSGGRARHQGVVMVGMGQK)
Lane 6 Peptide 8.4 at 13.3 $\mu$ M	(Biotin-SGSGGRPAHQGVVMVGMGQK)
Lane 7 Peptide 8.5 at 13.3 $\mu$ M	(Biotin-SGSGGRPRAQGVVMVGMGQK)
Lane 8 Peptide 8.6 at 13.3 $\mu$ M	(Biotin-SGSGAAAAAQGVVMVGMGQK)

*Fig. 11a**Fig 11b*

12/19

APPROVED	O.G. FIG.
BY	CLASS
DRAFTSMAN	SUBCLASS



*Fig. 11c*

13/19

APPROVED	D.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

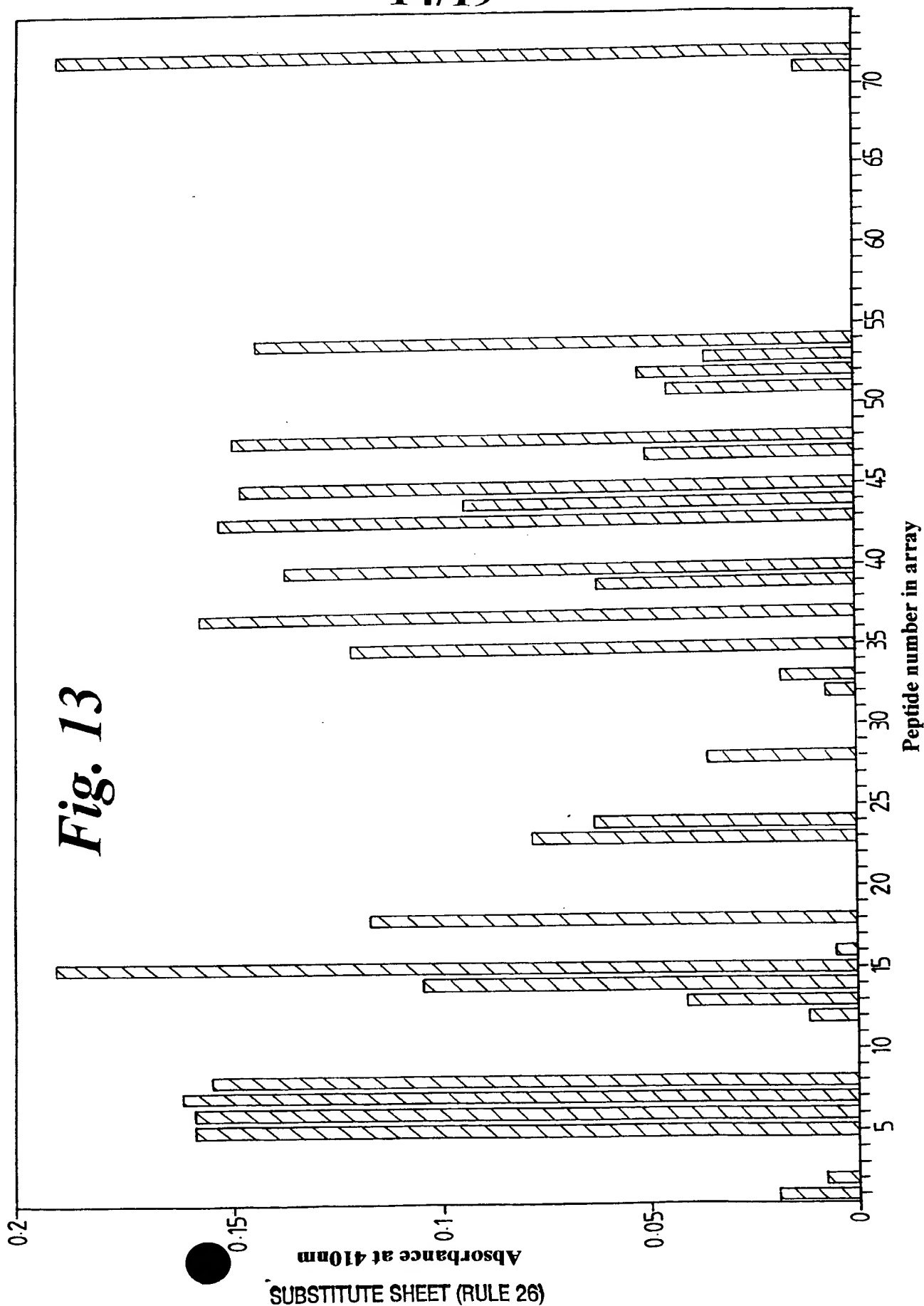
13 14 15 16 17 18

2 3 4 5 6 7 8 9 10 11 12

*Fig. 12*

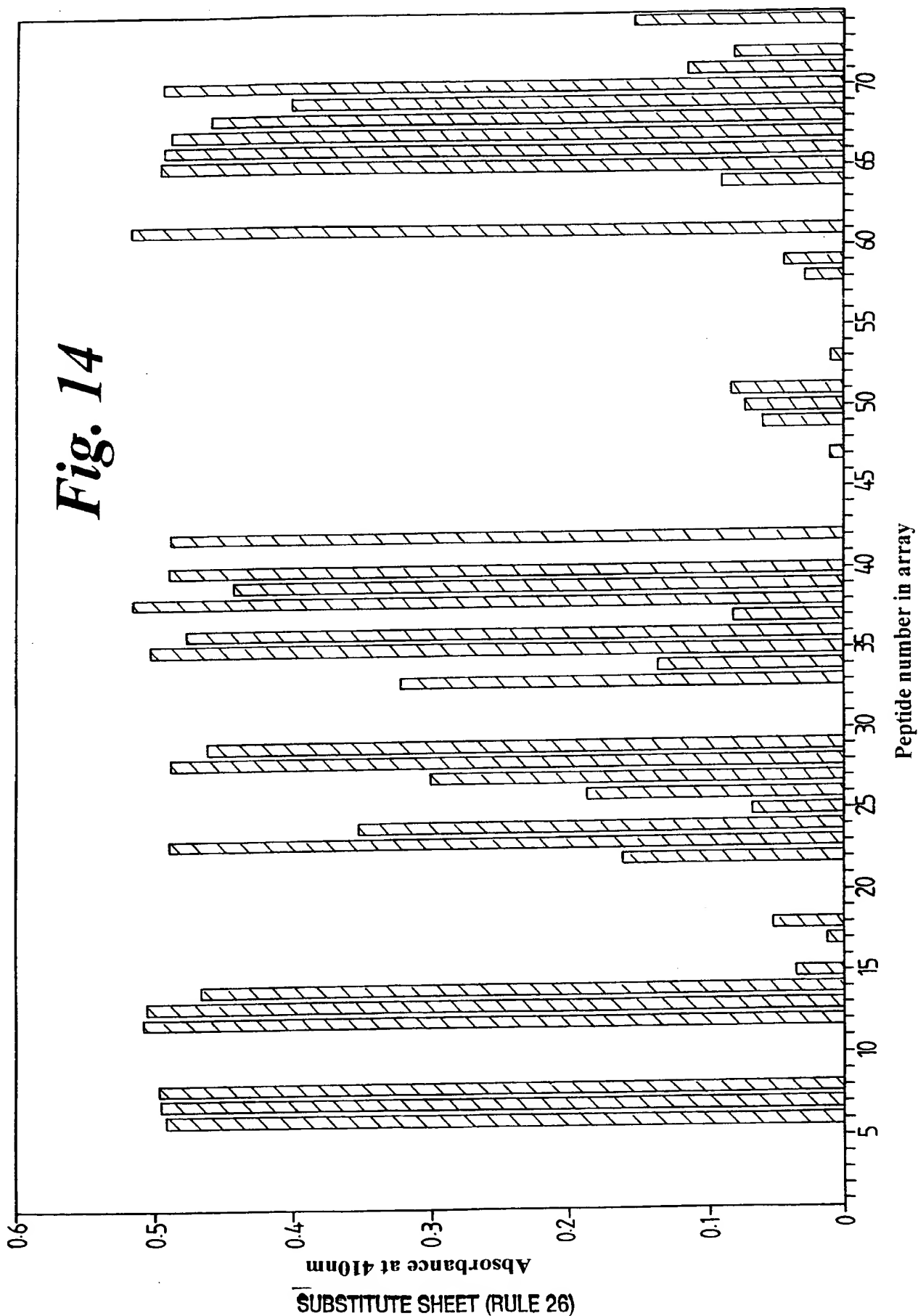
14/19

APPROVED	O.G. FIG.	
DY	CLASS	SUBCLASS
DRAFTSHAH		



15/19

Fig. 14



APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSHAH		

16/19

## TABLE 2

mouse beta actin - 15mer peptides with 5 residue overlap

1,	MDDDIAALVVDNGSG	= 1 - 15
2,	AALVVDNGSGMCKAG	= 6 - 20
3,	DNGSGMCKAGFAGDD	= 11 - 25
4,	MCKAGFAGDDAPRAV	= 16 - 30
5,	FAGDDAPRAVFPSIV	= 21 - 35
6,	APRAVFPSIVGRPRH	= 26 - 40
7,	FPSIVGRPRHQGVMV	= 31 - 45
8,	GRPRHQGVMVGMGQK	= 36 - 50
9,	QGVMVGMGQKDSYVG	= 41 - 55
10,	GMGQKDSYVGDEAQS	= 46 - 60
11,	DSYVGDEAQS KRGIL	= 51 - 65
12,	DEAQS KRGIL TLKYP	= 56 - 70
13,	KRGIL TLKYP IEHGI	= 61 - 75
14,	TLKYP IEHGI VTNWD	= 66 - 80
15,	IEHGI VTNWD DMEKI	= 71 - 85
16,	VTNWD DMEKI WHHTF	= 76 - 90
17,	DMEKI WHHTF FYNELR	= 81 - 95
18,	WHHTF FYNELR VAPEE	= 86 - 100
19,	FYNELR VAPEE HPVLL	= 91 - 105
20,	VAPEE HPVLL TEAPL	= 96 - 110
21,	HPVLL TEAPL NPKAN	= 101 - 115
22,	TEAPL NPKAN REKMT	= 106 - 120
23,	NPKAN REKMT QIMFE	= 111 - 125
24,	REKMT QIMFE TFNTP	= 116 - 130
25,	QIMFE TFNTP AMYVA	= 121 - 135
26,	TFNTP AMYVA IQAVL	= 126 - 140
27,	AMYVA IQAVL SLYAS	= 131 - 145
28,	IQAVL SLYAS GRRTG	= 136 - 150
29,	SLYAS GRRTG IVMDS	= 141 - 155
30,	GRRTG IVMDS GDGVT	= 146 - 160
31,	IVMDS GDGVT HTVPI	= 151 - 165
32,	GDGVT HTVPI YEGYA	= 156 - 170
33,	HTVPI YEGYA ALPHA I	= 161 - 175
34,	YEGYA ALPHA IRLDL	= 166 - 180
35,	ALPHA IRLDL AGRDL	= 171 - 185
36,	IRLDL AGRDL TDYLM	= 176 - 190
37,	AGRDL TDYLM KILTE	= 181 - 195
38,	TDYLM KILTE RGYSF	= 186 - 200
39,	KILTE RGYSF TTTAE	= 191 - 205
40,	RGYSF TTTAE REIVR	= 196 - 210
41,	TTTAE REIVR DIKEK	= 201 - 215
42,	REIVR DIKEK LCYVA	= 206 - 220
43,	DIKEK LCYVA LD FEQ	= 211 - 225
44,	LCYVA LD FEQ EMATA	= 216 - 230



## 17/19

45, LDFEQEMATAASSSS = 221 - 235  
 46, EMATAASSSSLEKSY = 226 - 240  
 47, ASSSSLEKSYELPDG = 231 - 245  
 48, LEKSYELPDGQVITI = 236 - 250  
 49, ELPDGQVITIGNERF = 241 - 255  
 50, QVITIGNERFRCPEA = 246 - 260  
 51, GNERFRCPEALFQPS = 251 - 265  
 52, RCPEALFQPSFLGME = 256 - 270  
 53, LFQPSFLGMESCGIH = 261 - 275  
 54, FLGMESCGIHETTFN = 266 - 280  
 55, SCGIHETTFNSIMKC = 271 - 285  
 56, ETTFNSIMKCDVDIR = 276 - 290  
 57, SIMKCDVDIRKDLYA = 281 - 295  
 58, DVDIRKDLYANTVLS = 286 - 300  
 59, KDLYANTVLSGGTTM = 291 - 305  
 60, NTVLSGGTTMYPGIA = 296 - 310  
 61, GGTMYPGIADRMQK = 301 - 315  
 62, YPGIADRMQKEITAL = 306 - 320  
 63, DRMQKEITALAPSTM = 311 - 325  
 64, EITALAPSTMKIKII = 316 - 330  
 65, APSTMKIKIIAPPER = 321 - 335  
 66, KIKIIAPPERKYSVW = 326 - 340  
 67, APPERKYSVWIGGSI = 331 - 345  
 68, KYSVWIGGSILASLS = 336 - 350  
 69, IGGSILASLSTFQQM = 341 - 355  
 70, LASLSTFQQMWISKQ = 346 - 360  
 71, TFQQMWISKQEYDES = 351 - 365  
 72, WISKQEYDESGPSIV = 356 - 370  
 73, EYDESGPSIVHRKCF = 361 - 375  
 74, GGGGGGPSIVHRKCF = 366 - 375  
 75, GGGGGGGGGHHRKCF = 371 - 375

Other peptides to include:

76, KYSVWIGGSILASLS

alpha helix in subdomain 1 of rabbit alpha actin-contains  
two hydrophobic residues accessible to solvent  
(residues S338 - S348)

77, PRHQVMVGMGQKDS

loop in subdomain 2 of rabbit alpha actin-major  
interaction site with DNase I  
(residues P38 - S52)

78, IVLDSGDGVTHNVPI

beta stands in subdomain 3 of rabbit alpha actin  
(residues G150 - Y166)

79, LVCDNGSGLVKAGFA

## 18/19

analagous beta strand motif in subdomain 1 of rabbit  
alpha actin  
(residues L8 - F21)

80, LFQPSFIGMESAGIH  
loop in subdomain 4 of rabbit alpha actin-involved in  
contact across helix axis in F-actin  
(residues F262 - L274)

81, TTAEREIVRDIKEKL  
Alpha helix in subdomain 4 of rabbit alpha actin-minor  
interaction site with DNase I  
(residues T203 - L216)

82, YVGDEAQSKRGILT  
beta alpha beta unit in subdomain 2 of rabbit alpha  
actin-minor interaction site with DNase I/  
hexokinase-like unit  
(residues K61 - L65)

83, VMSGGTTMYPGIADR  
loop in subdomain 3 of rabbit alpha actin-forms pocket  
for adenine base of nucleotide  
(residues S300 - I309)

84, KIKIIAPPERKYSVW  
beta strand and loop in subdomain 3 of rabbit alpha  
actin-forms pocket for adenine base of nucleotide  
(residues K328 - S338)

85, GFAGDDAPRAVFPSI  
loop in subdomain 1 of rabbit alpha actin-central contact  
region of myosin on 'flat' side of actin  
(residues F21 - P32)

86, YNELRVAPEEHPTLL  
loop in subdomain 1 of rabbit alpha actin-contact region  
of myosin on 'flat' side of actin  
(residues N92 - T103)

87, TFQQMWITKQEYDEA  
alpha helices in subdomain 1 of rabbit alpha actin-bind  
myosin chains  
(residues S348 - A365)

19/19

88, DEDETTALVCDNGSG

N-terminal 15 residues of rabbit alpha actin-important in  
binding myosin  
(residues D1 - G15)

89, EYDEAGPSIVHRKCF

C-terminal 15 residues of rabbit alpha actin  
(residues E361 - F375)

90, SKQEYDESGPSIVHR

truncated C-terminus of mouse beta actin  
(residues S358 - R372)

91, ILTERGYSFVTTAER

loop in subdomain 4 of rabbit alpha actin-analogous to  
DNase I-binding loop in subdomain 2  
(residues T194 - T203)

92, ALDFENEMATAASSS

alpha helix flanked by loops in subdomain 4 of rabbit  
alpha actin  
(residues F223 - A230)

93, WDDMEKIWHHTFYNE

alpha helix in subdomain 1 of rabbit alpha actin  
(residues W79 - N92)

94, +ve control for 91a = STDLVAKLRAFHNEA